

RAW SEQUENCE LISTING  
PATENT APPLICATION US/08/320,157DATE: 03/17/95  
TIME: 09:29:28

INPUT SET: S2805.raw

This Raw Listing contains the General  
Information Section and up to the first 5 pages.

ENTERED

## SEQUENCE LISTING

1  
2  
3 (1) General Information:  
4  
5 (i) APPLICANT: KIEFER, MICHAEL C.  
6 BARR, PHILIP J.  
7  
8 (ii) TITLE OF INVENTION: NOVEL APOPTOSIS-MODULATING PROTEINS, DNA  
9 ENCODING THE PROTEINS AND METHODS OF USE THEREOF  
10  
11 (iii) NUMBER OF SEQUENCES: 22  
12  
13 (iv) CORRESPONDENCE ADDRESS:  
14 (A) ADDRESSEE: MORRISON & FOERSTER  
15 (B) STREET: 755 Page Mill Road  
16 (C) CITY: Palo Alto  
17 (D) STATE: California  
18 (E) COUNTRY: USA  
19 (F) ZIP: 94304-1018  
20  
21 (v) COMPUTER READABLE FORM:  
22 (A) MEDIUM TYPE: Floppy disk  
23 (B) COMPUTER: IBM PC compatible  
24 (C) OPERATING SYSTEM: PC-DOS/MS-DOS  
25 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30  
26  
27 (vi) CURRENT APPLICATION DATA:  
28 (A) APPLICATION NUMBER: US 08/320,157  
29 (B) FILING DATE: 07-OCT-1994  
30 (C) CLASSIFICATION:  
31  
32 (viii) ATTORNEY/AGENT INFORMATION:  
33 (A) NAME: LEHNHARDT, SUSAN K.  
34 (B) REGISTRATION NUMBER: 33,943  
35 (C) REFERENCE/DOCKET NUMBER: 23647-20007.20  
36  
37 (ix) TELECOMMUNICATION INFORMATION:  
38 (A) TELEPHONE: (415) 813-5600  
39 (B) TELEFAX: (415) 494-0792  
40 (C) TELEX: 706141  
41  
42  
43 (2) INFORMATION FOR SEQ ID NO:1:  
44  
45 (i) SEQUENCE CHARACTERISTICS:  
46 (A) LENGTH: 8 amino acids

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47 (B) TYPE: amino acid  
48 (C) STRANDEDNESS: single  
49 (D) TOPOLOGY: linear  
50  
51  
52  
53  
54  
55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:  
56  
57 Asp Trp Gly Arg Val Val Ala Ile  
58 1 5  
59  
60 (2) INFORMATION FOR SEQ ID NO:2:  
61  
62 (i) SEQUENCE CHARACTERISTICS:  
63 (A) LENGTH: 36 base pairs  
64 (B) TYPE: nucleic acid  
65 (C) STRANDEDNESS: single  
66 (D) TOPOLOGY: linear  
67  
68  
69  
70 (ix) FEATURE:  
71 (A) NAME/KEY: misc\_difference  
72 (B) LOCATION: replace(23, "")  
73 (D) OTHER INFORMATION: /note= "This position is inosine."  
74  
75 (ix) FEATURE:  
76 (A) NAME/KEY: misc\_difference  
77 (B) LOCATION: replace(27, "")  
78 (D) OTHER INFORMATION: /note= "This position is inosine."  
79  
80  
81 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:  
82  
83 AGATCTGAAT TCAACTTGGG GGNCAGNAGT NGTNGC 36  
84  
85 (2) INFORMATION FOR SEQ ID NO:3:  
86  
87 (i) SEQUENCE CHARACTERISTICS:  
88 (A) LENGTH: 11 amino acids  
89 (B) TYPE: amino acid  
90 (C) STRANDEDNESS: single  
91 (D) TOPOLOGY: linear  
92  
93  
94  
95  
96  
97 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:  
98  
99 Asp Trp Gly Gly Gln Glu Asn Asp Gln Ile Trp

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100      1          5          10
101
102 (2) INFORMATION FOR SEQ ID NO:4:
103
104 (i) SEQUENCE CHARACTERISTICS:
105 (A) LENGTH: 29 base pairs
106 (B) TYPE: nucleic acid
107 (C) STRANDEDNESS: single
108 (D) TOPOLOGY: linear
109
110
111
112 (ix) FEATURE:
113 (A) NAME/KEY: misc_difference
114 (B) LOCATION: replace(6, "")
115 (D) OTHER INFORMATION: /note= "This position is inosine."
116
117 (ix) FEATURE:
118 (A) NAME/KEY: misc_difference
119 (B) LOCATION: replace(9, "")
120 (D) OTHER INFORMATION: /note= "This position is inosine."
121
122
123 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
124
125 AGGGTNGGNG GNACNAGAGA CATCTAGGT 29
126
127 (2) INFORMATION FOR SEQ ID NO:5:
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129 (i) SEQUENCE CHARACTERISTICS:
130 (A) LENGTH: 41 base pairs
131 (B) TYPE: nucleic acid
132 (C) STRANDEDNESS: single
133 (D) TOPOLOGY: linear
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135
136
137 (ix) FEATURE:
138 (A) NAME/KEY: misc_difference
139 (B) LOCATION: replace(19, "")
140 (D) OTHER INFORMATION: /note= "This position is inosine."
141
142 (ix) FEATURE:
143 (A) NAME/KEY: misc_difference
144 (B) LOCATION: replace(22, "")
145 (D) OTHER INFORMATION: /note= "This position is inosine."
146
147
148 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
149
150 AGATCTAAGC TTGTCCCAAC CNCCNTGNTC CTTGAGATCC A 41
151
152 (2) INFORMATION FOR SEQ ID NO:6:
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153  
154 (i) SEQUENCE CHARACTERISTICS:  
155 (A) LENGTH: 2094 base pairs  
156 (B) TYPE: nucleic acid  
157 (C) STRANDEDNESS: single  
158 (D) TOPOLOGY: linear  
159  
160  
161  
162 (ix) FEATURE:  
163 (A) NAME/KEY: CDS  
164 (B) LOCATION: 201..833  
165  
166  
167 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:  
168  
169 GAGGATCTAC AGGGGACAAG TAAAGGCTAC ATCCAGATGC CGGGAATGCA CTGACGCCCA 60  
170  
171 TTCCTGGAAA CTGGGCTCCC ACTCAGCCCC TGGGAGCAGC AGCCGCCAGC CCCTCGGACC 120  
172  
173 TCCATCTCCA CCCTGCTGAG CCACCCGGGT TGGGCCAGGA TCCCGGCAGG CTGATCCCGT 180  
174  
175 CCTCCACTGA GACCTGAAAA ATG GCT TCG GGG CAA GGC CCA GGT CCT CCC 230  
176 Met Ala Ser Gly Gln Gly Pro Gly Pro Pro  
177 1 5 10  
178  
179 AGG CAG GAG TGC GGA GAG CCT GCC CTG CCC TCT GCT TCT GAG GAG CAG 278  
180 Arg Gln Glu Cys Gly Glu Pro Ala Leu Pro Ser Ala Ser Glu Glu Gln  
181 15 20 25  
182  
183 GTA GCC CAG GAC ACA GAG GAG GTT TTC CGC AGC TAC GTT TTT TAC CGC 326  
184 Val Ala Gln Asp Thr Glu Glu Val Phe Arg Ser Tyr Val Phe Tyr Arg  
185 30 35 40  
186  
187 CAT CAG CAG GAA CAG GAG GCT GAA GGG GTG GCT GCC CCT GCC GAC CCA 374  
188 His Gln Gln Glu Gln Glu Ala Glu Gly Val Ala Ala Pro Ala Asp Pro  
189 45 50 55  
190  
191 GAG ATG GTC ACC TTA CCT CTG CAA CCT AGC AGC ACC ATG GGG CAG GTG 422  
192 Glu Met Val Thr Leu Pro Leu Gln Pro Ser Ser Thr Met Gly Gln Val  
193 60 65 70  
194  
195 GGA CGG CAG CTC GCC ATC ATC GGG GAC GAC ATC AAC CGA CGC TAT GAC 470  
196 Gly Arg Gln Leu Ala Ile Ile Gly Asp Asp Ile Asn Arg Arg Tyr Asp  
197 75 80 85 90  
198  
199 TCA GAG TTC CAG ACC ATG TTG CAG CAC CTG CAG CCC ACG GCA GAG AAT 518  
200 Ser Glu Phe Gln Thr Met Leu Gln His Leu Gln Pro Thr Ala Glu Asn  
201 95 100 105  
202  
203 GCC TAT GAG TAC TTC ACC AAG ATT GCC ACC AGC CTG TTT GAG AGT GGC 566  
204 Ala Tyr Glu Tyr Phe Thr Lys Ile Ala Thr Ser Leu Phe Glu Ser Gly  
205 110 115 120



**NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES**

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 CFR 1.821 - 1.825 for the following reason(s):

- ☒ 1. This application clearly fails to comply with the requirements of 37 CFR 1.821 - 1.825. Applicant's attention is directed to these regulations, published at 1114 OG 29, May 15, 1990 and at 55 FR 18230, May 1, 1990.
- ☐ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 CFR 1.821(c).
- ☐ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 CFR 1.821(e).
- ☐ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 CFR 1.822 and/or 1.823, as indicated on the attached marked-up copy of the "Raw Sequence Listing."
- ☐ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A substitute computer readable form must be submitted as required by 37 CFR 1.825(d).
- ☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 CFR 1.821(e).
- ☐ 7. Other: \_\_\_\_\_

**Applicant must provide:**

- ☒ An initial or substitute computer readable form (CRF) copy of the "Sequence Listing"
- ☒ An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification
- ☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 CFR 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d)

For questions regarding compliance with these requirements, please contact:

For Rules Interpretation, call (703) 308-1123  
For CRF submission help, call (703) 308-4212  
For PatentIn software help, call (703) 308-6856

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